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COW4

at the National Center for Biotechnology Information (NCBI) world wide web site. BLAST nucleotide searches can be performed with the NBLAST program (designated "blastn" at the NCBI web site), using the following parameters: gap penalty = 5; gap extension penalty = 2; mismatch penalty = 3; match reward = 1; expectation value 10.0; and word size = 11 to obtain nucleotide sequences homologous to a nucleic acid described herein. BLAST protein searches can be performed with the XBLAST program (designated "blastn" at the NCBI web site) or the NCBI "blastp" program, using the following parameters: expectation value 10.0, BLOSUM62 scoring matrix to obtain amino acid sequences homologous to a protein molecule described herein. --

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Please delete the paragraph commencing on page 24, line 7, ~~and ending on page 24, line 23,~~ and insert the following paragraph in place thereof:

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A2

-- To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997, Nucleic Acids Res. 25:3389-3402). Alternatively, PSI-Blast or PHI-Blast can be used to perform an iterated search which detects distant relationships between molecules (*id.*) and relationships between molecules which share a common pattern. When utilizing BLAST, Gapped BLAST, PSI-Blast, and PHI-Blast programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used. See world wide web site for the government National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health. --

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Please delete the paragraph commencing on page 38, line 2, and ending on page 38, line 22, and insert the following paragraph in place thereof:

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A3

-- The skilled artisan would appreciate, based upon the disclosure provided herein, the wide plethora of nucleic acids can be used as a target nucleic acid to produce the nucleic acid reference standard of the invention. That is, virtually any nucleic acid sequence of interest can be introduced into the construct using the methods disclosed herein to produce the claimed reference standard. More specifically, the invention encompasses a nucleic reference standard comprising a wide plethora of target nucleic acids, including, but not limited to, a methyltetrahydrofolate reductase gene, a beta cystathionase synthetase nucleic acid, nucleic acid related to coagulation factors including Factor II, Factor VII, Factor VIII, and Factor IX, a nucleic acid associated with prothrombin, nucleic acid containing translocations related to